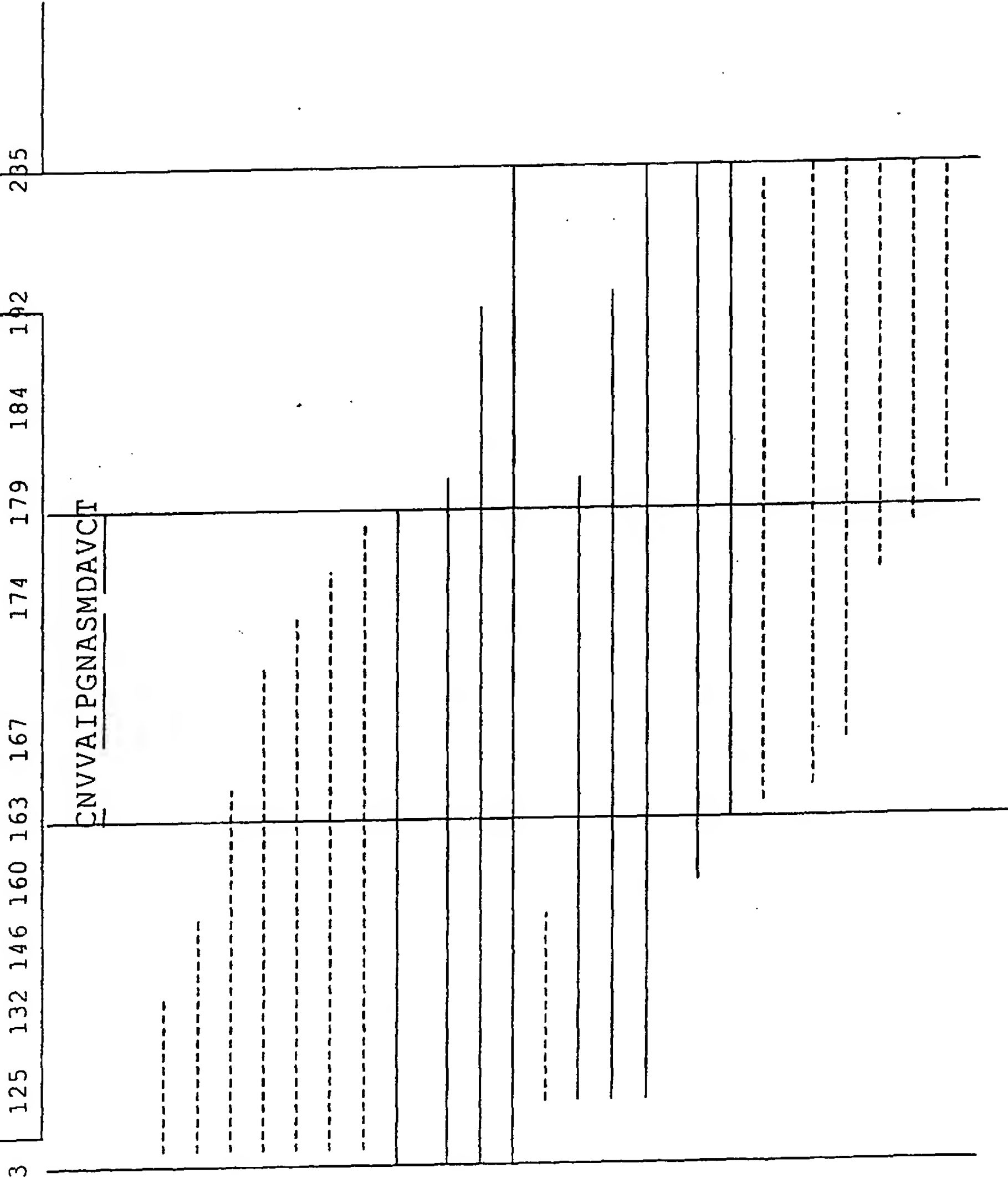


FIG. 1

(Soluble Receptor)

TM

...AQV.F...T...T.HQICNVVAIPGNASMDAVCTSTSTPT...V.....DEALPVGLI



3-132
3-146
3-164
3-170
3-173
3-176
3-178
3-179
3-180
3-192
3-235
125-146
125-180
125-192
125-235
160-235
163-235
164-235
165-235
167-235
175-235
178-235
181-235

FIG. 2

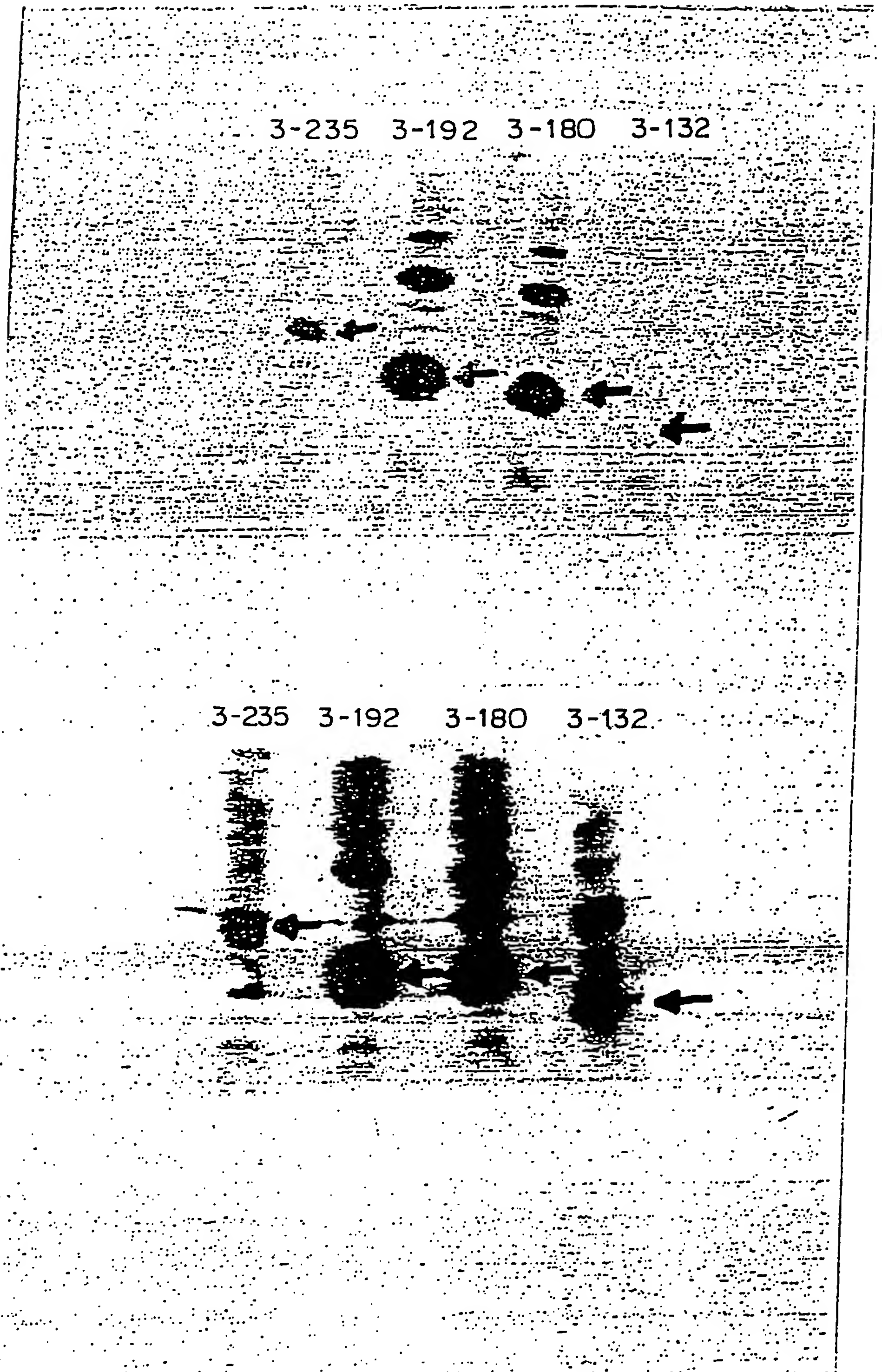
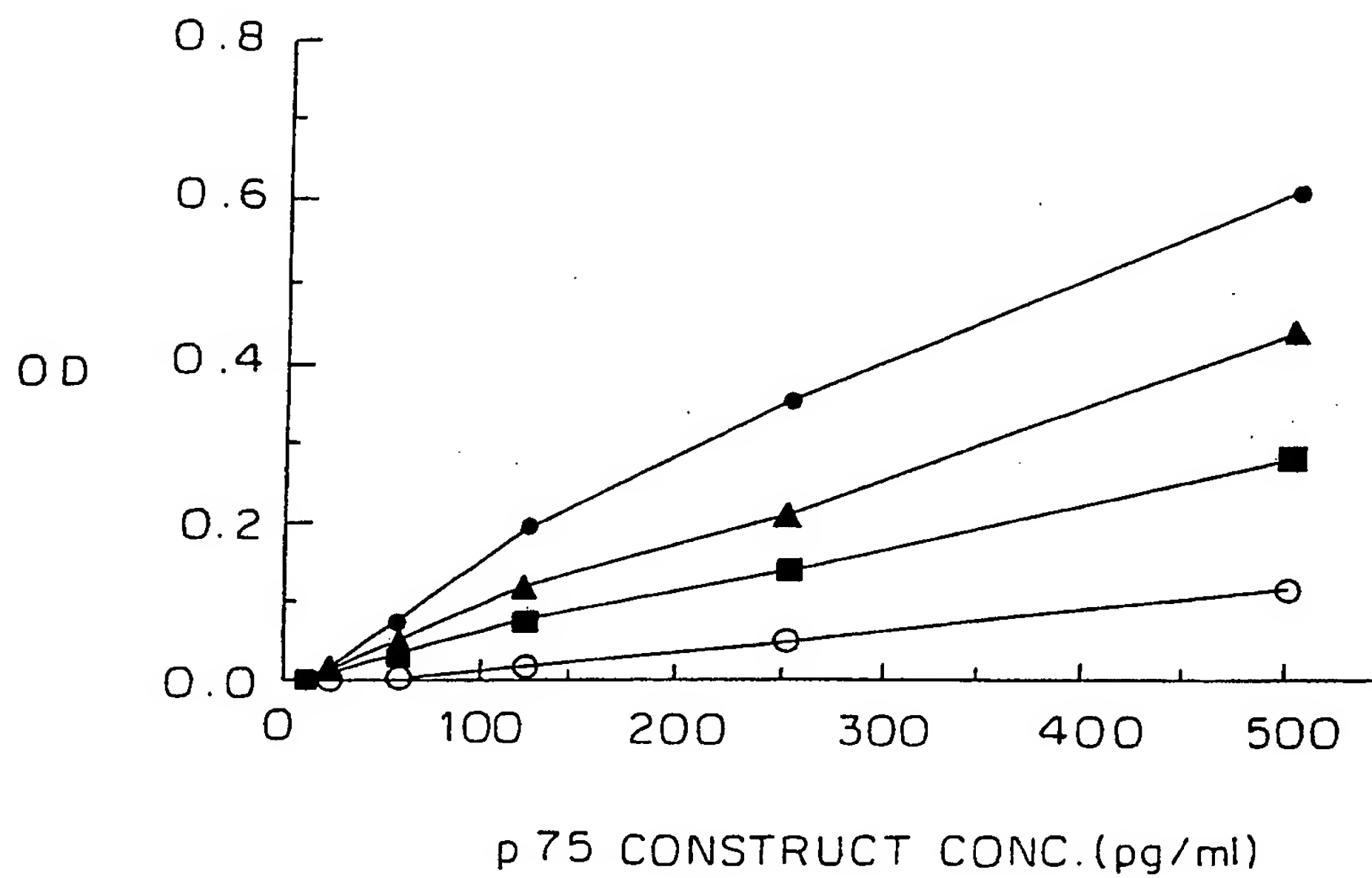


FIG. 3

INHIBITION OF #32 AND p75 INTERACTION BY
THE EPITOPE PEPTIDE



- no pept
- ▲— 1 ug/ml
- 10 ug/ml
- 100 ug/ml

FIG. 4

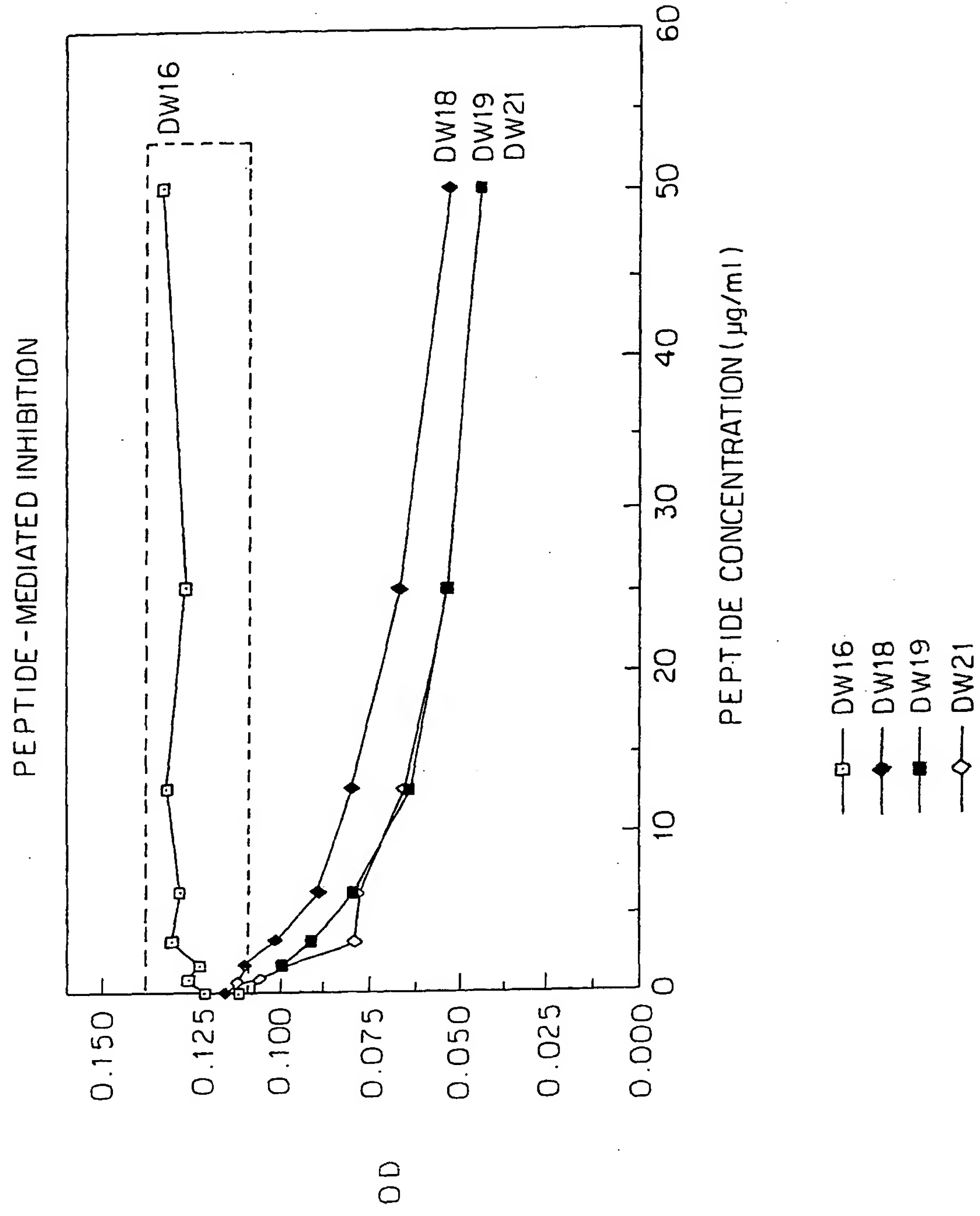


FIG. 5A

1 gcgagcgag cggagcctgg agagaaggcg ctgggctgag agggcgaggg ggcgggcaa cggaccccc
81
ccgcacccc atg gcg ccc gtc gcc gtc tgg gcc ctg ggc gga ctg gag ctc tgg gct gcg
Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
147 -22
gcg cac gcc ttg ccc gcc cag gtg gca ttt aca ccc tac gcc cgg gag ccc ggg agc aca tgc cgg
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser Thr Cys Arg
213 -1 +1
ctc aga gaa tac tat gac cag aca gct cag atg tgc tgc agc aaa tgc tgc cgg ggc caa cat gca
10
Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala
279 32
aaa gtc ttc tgt acc aag acc tgc gac acc gtg tgt gac tcc tgt gag gac agc aca tac acc cag
Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln
345 54
ctc tgg aac tgg gtt ccc gag tgc ttg agc tgt gcc tcc cgc tgt agc tct gac cag gtg gaa act
Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr
411 76
caa gcc tgc act cgg gaa cag aac cgc atc tgc acc tgc agc ccc gcc tgg tac tgc gcg ctg agc
Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser
477 98
aag cag gag ggg tgc cgg ctg tgc gcg cgg ctg cgc aag tgc cgc cgg gcc ttc gcc gtg gcc aga
Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala Arg
543 120
cca gga act gaa aca tca gac gtg tgc aag ccc tgt gcc cgg ggg acg ttc ttc aac acg act
Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr
609 142
tca tcc acg gat att tgc agg ccc cac cag atc tgt aac gtg ggc gcc atc ccc ggg aat gca agc
Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser
675 164
atg gat gca gtc tgc acg tcc acg tcc ccc acc cgg agc atg gcc cca ggg gca gta cac tta ccc
Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala Pro Gly Ala Val His Leu Pro
741 186

TBPII

FIG. 5B

TRANSMEMBRANE		DOMAIN	
cag cca gtg tcc aca cga tcc caa cac acg cag cca act cca gaa ccc agc act gct cca agc acc			
Gln Pro Val Ser Thr Arg Ser Gln Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr			
807	208		
tcc ttc ctg ctc cca atg ggc ccc agc ccc cca gct gaa ggg agc act ggc gac		ttc gct ctt cca	
Ser Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp		Phe Ala Leu Pro	
873	230		
ggt gga ctg att gtg ggt gtg aca gcc ttg ggt cta cta ata gga gtg gac tgc atc			
Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly Leu Ile Ile Gly Val Val Asn Cys Val Ile			
939	252		
atg acc cag gtg aaa aag aag ccc ttg tgc ctg cag aga gaa gcc aag gtg cct cac ttg cct gcc			
Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro Ala			
1005	274		
gat aag gcc cgg ggt aca cag ggc ccc gag cag cag cac ctg ctg atc aca ggc ccg agc tcc agc			
Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu Ile Thr Ala Pro Ser Ser Ser			
1071	296		
agc agc tcc ctg gag agc tgc gcc agt gcg ttg gac aga agg gcg ccc act cgg aac cag cca cag			
Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln			
1137	318		
gca cca gcc gtg gag gcc agt ggg gcc gcg gag gcc agc acc ggg agc tca gat tct tcc			
Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln			
1203	340		
ctt ggt ggc cat ggg acc cag gtc aat gtc acc tgc atc gtg aac gtc tgt agc agc tct gac cac			
Ala Pro Gly Val Glu Ala Ser Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Asp His			
1269	362		
agc tca cag tgc tcc tcc caa gcc agc tcc aca atg gga gac aca gat tcc agc ccc tgc gag tcc			
Ser Ser Gln Cys Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser			
1335	384		
ccg aag gac gag cag gtc ccc ttc tcc aag gag gaa tgt gcc ttt cgg tca cag ctg gag acg cca			
Pro Lys Asp Glu Gln Val Pro phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu Thr Pro			
1401	406		
gag acc ctg ctg ggg agc acc gaa gag aag ccc ctg ccc ttt gga gtg cct gat gct ggg atg aag			
Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys			
1467	428		
ccc agt taa ccaggccggt gtgggctgtg tcgtagccaa ggtgggctga gccctggcag gatgaccctg cgaaggggc			
Pro Ser End			
	439		

FIG. 5C

1545

cctggtcctt ccaggccccc accactagga ctctgaggct cttctgggc caagtcctc tagtgccctc cacagccgca
gcctccctct gacctgcagg ccaagagcag aggcagcgag ttggggaaag cctctgctgc catgggtgtgt ccctctcgga
aggctggctg ggcattggacg ttccggggcat gctggggcaa gtccctgact ctctgtgacc tgccccgccc agctgcacct
gccagcctgg ctcttgagc ccttgggttt ttgtttgtt ttgtttgtt tctccccctg tgctctgccc
agctctggct tccagaaaac ccagcatcc ttctctgcag aggggctttc tggagaggag ggatgctgcc tgagtcaccc
atgaagacag gacagtgtt ctgccctgagg cagagactgc gggatggctc tggggctctg tgtagggagg agtgggcagc
cctgtaggga acgggtcct tcaagttagc tcaggaggct tggaaagcat cacctcaggc caggtgcagt ggctcacgcc
tatgatccca gcactttggg aggcagggc gggtggatca cctgaggtta ggagttcgag accagcctgg ccaacatggt
aaaaccccat ctctactaaa aatacagaaa ttagccgggc3683

acctcaggc caggtgcagt ggctcacgcc

2075

FIG. 6

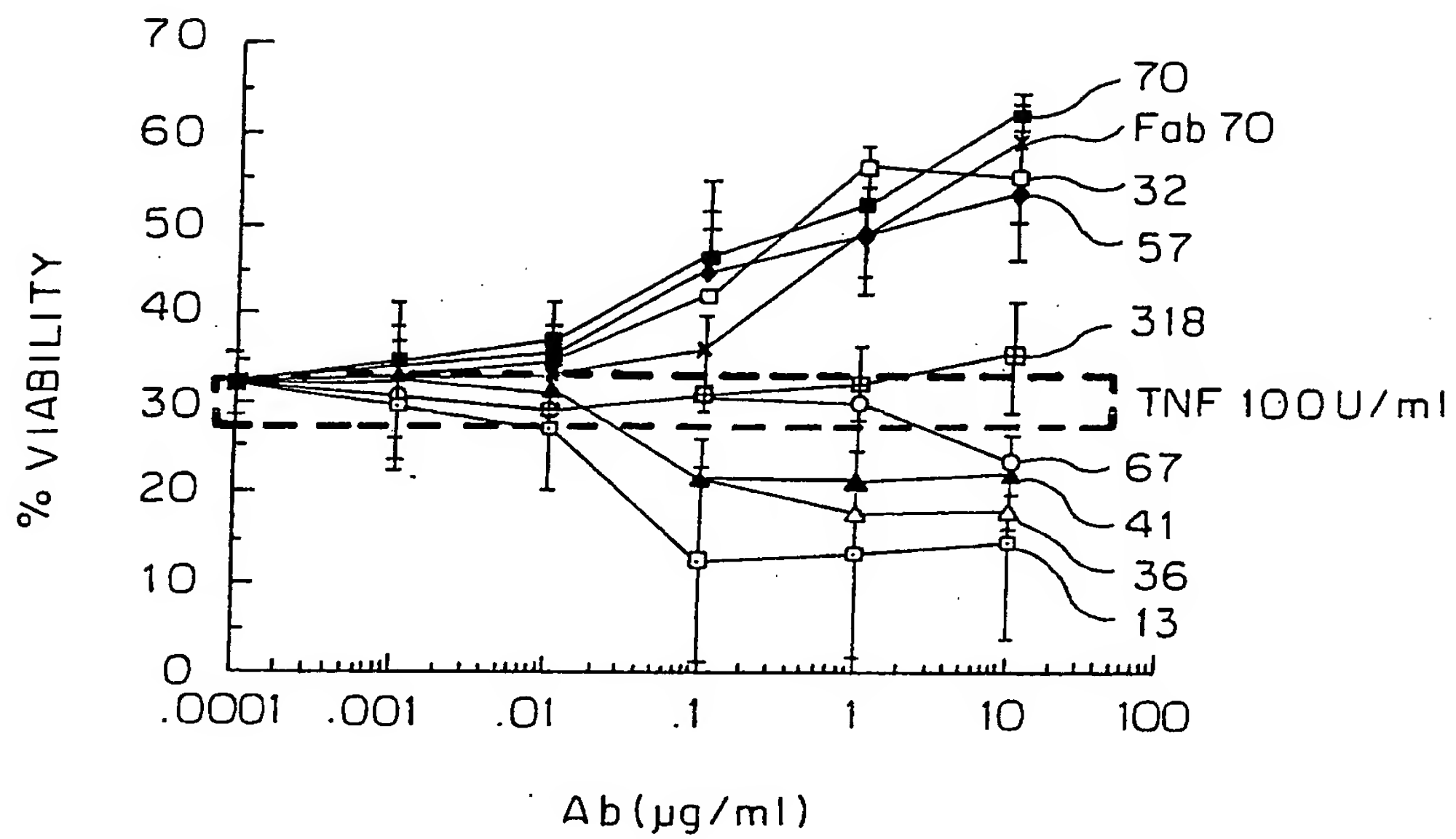


FIG. 7

U937 - PROTECTION

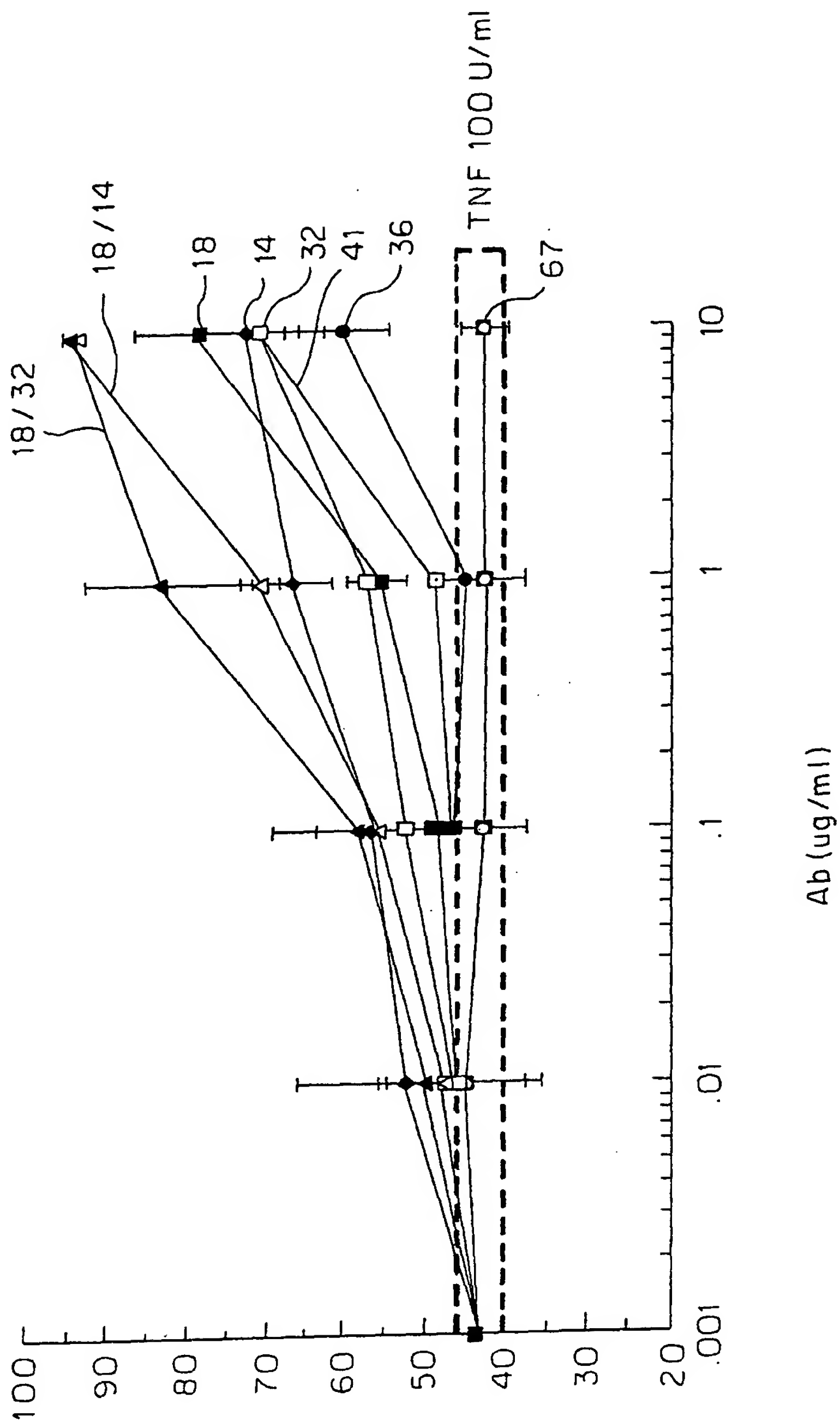


FIG. 8A

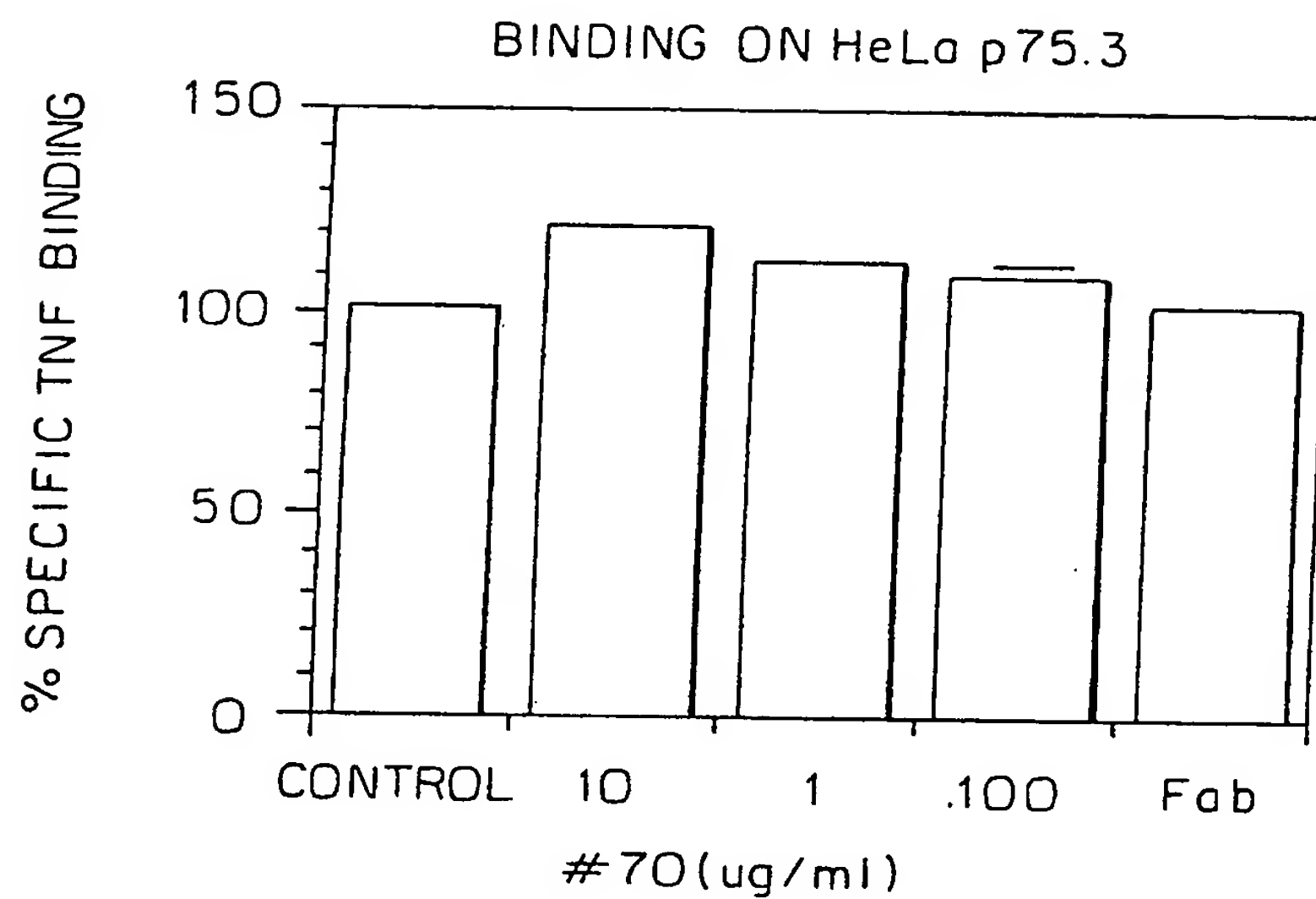


FIG. 8B

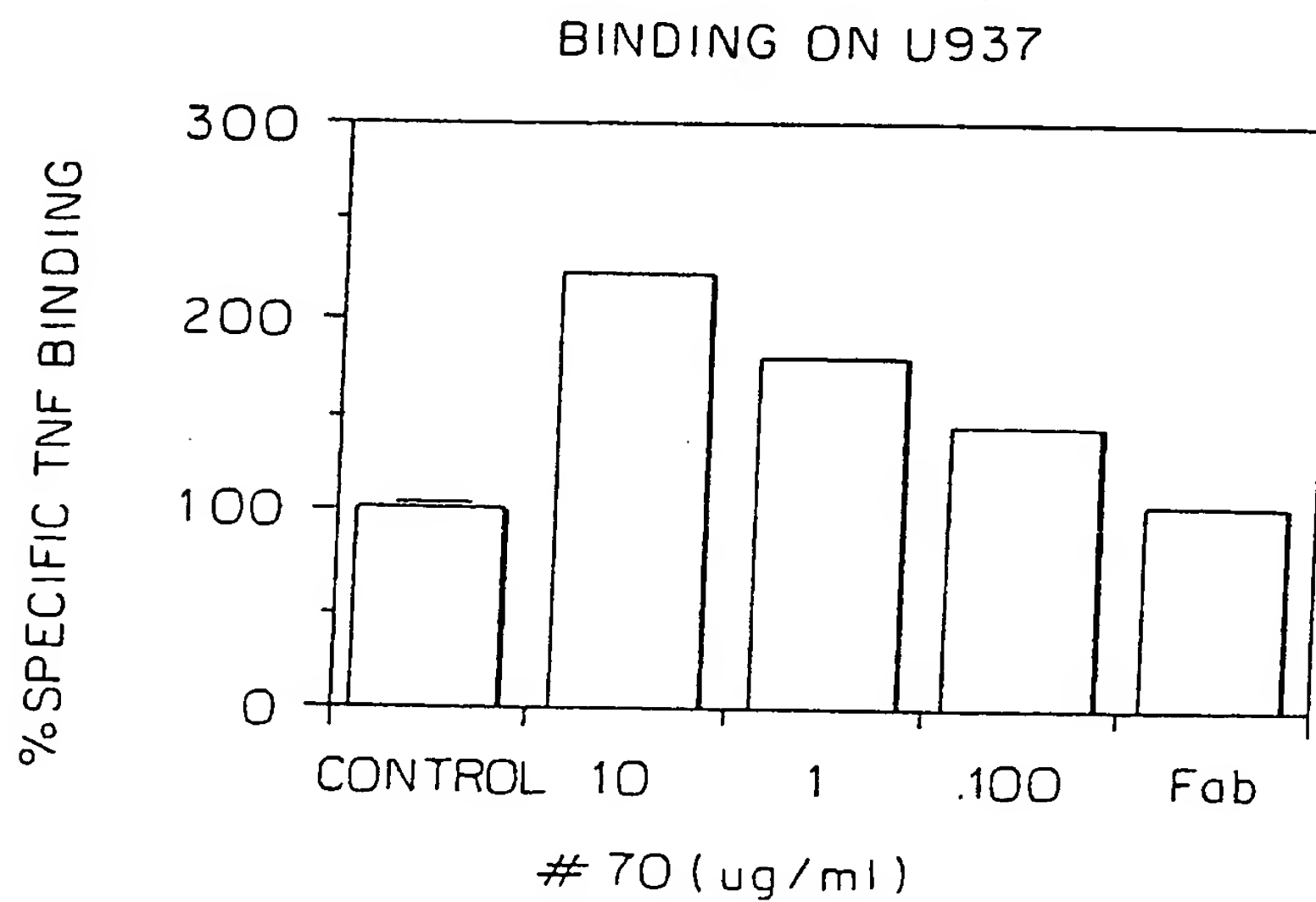


FIG. 9A

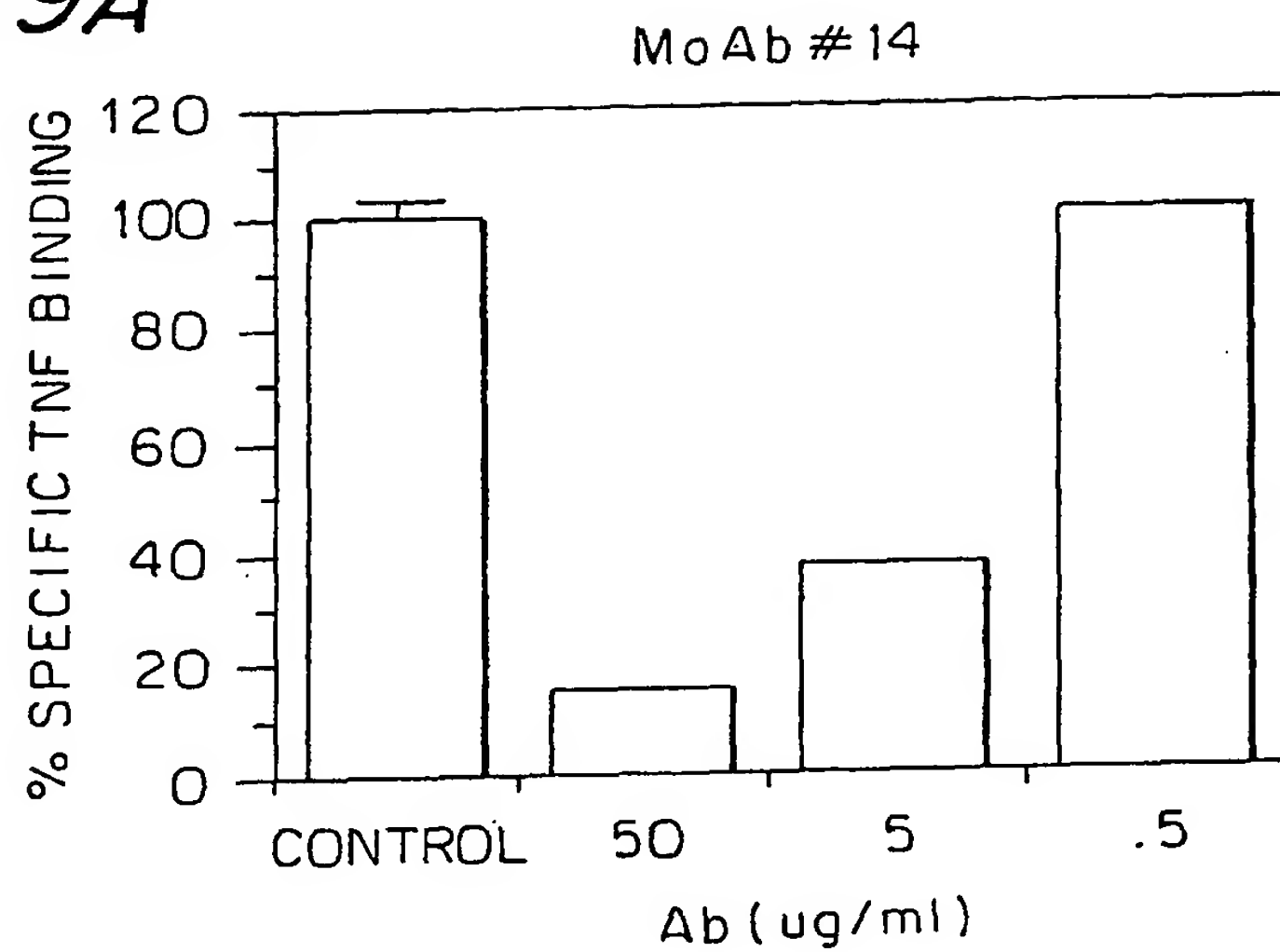


FIG. 9B

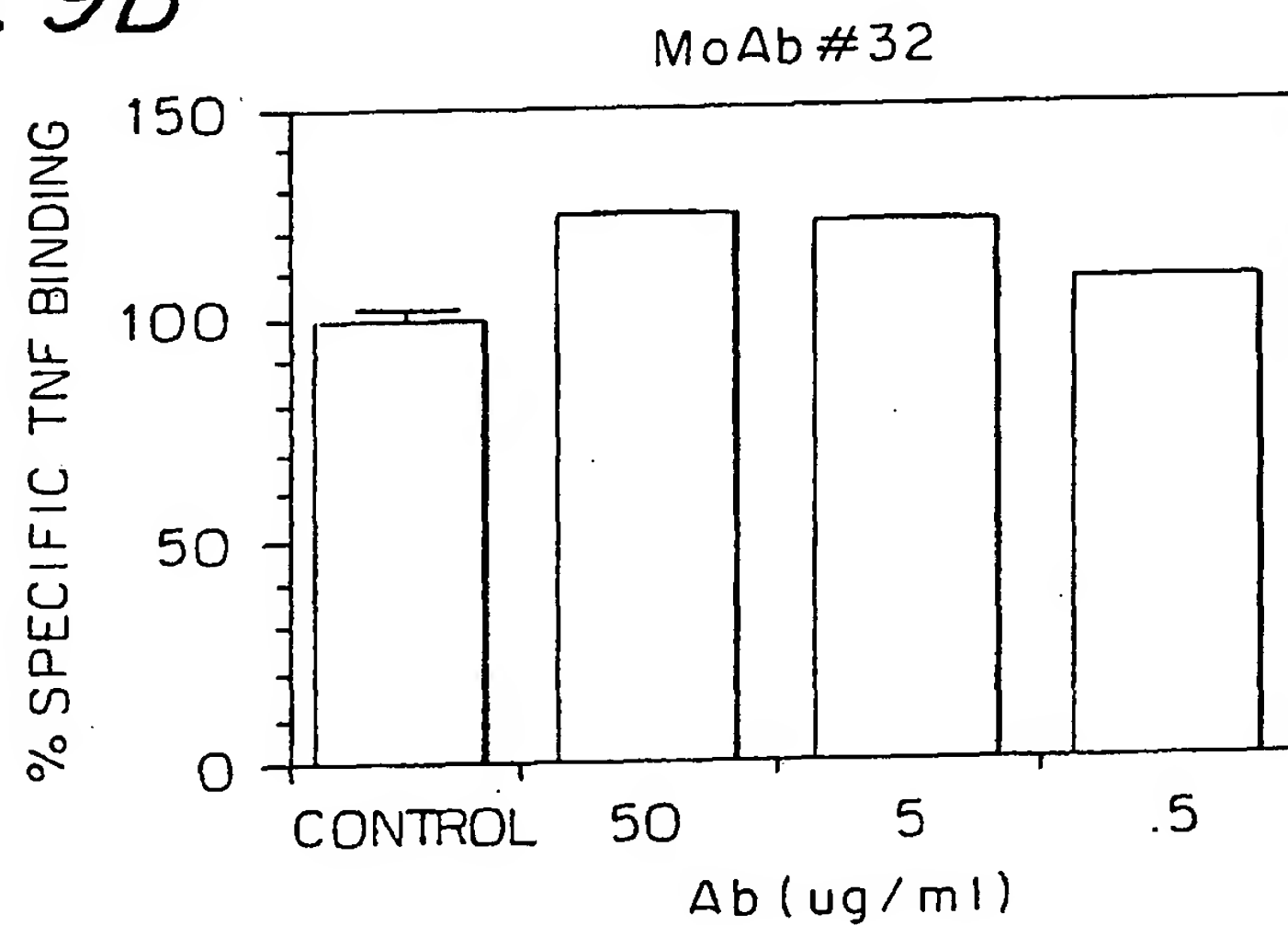


FIG. 9C

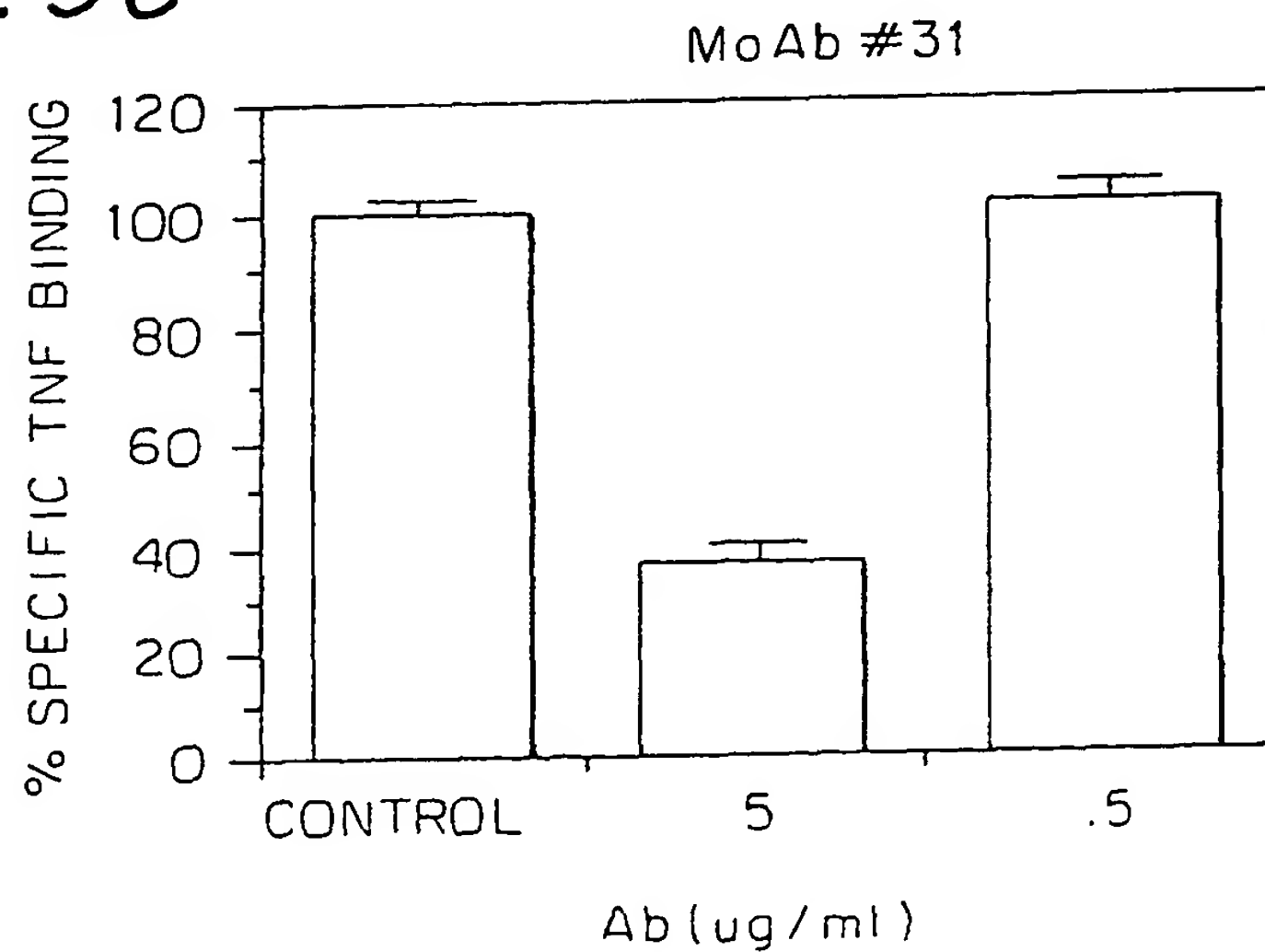


FIG. 9D

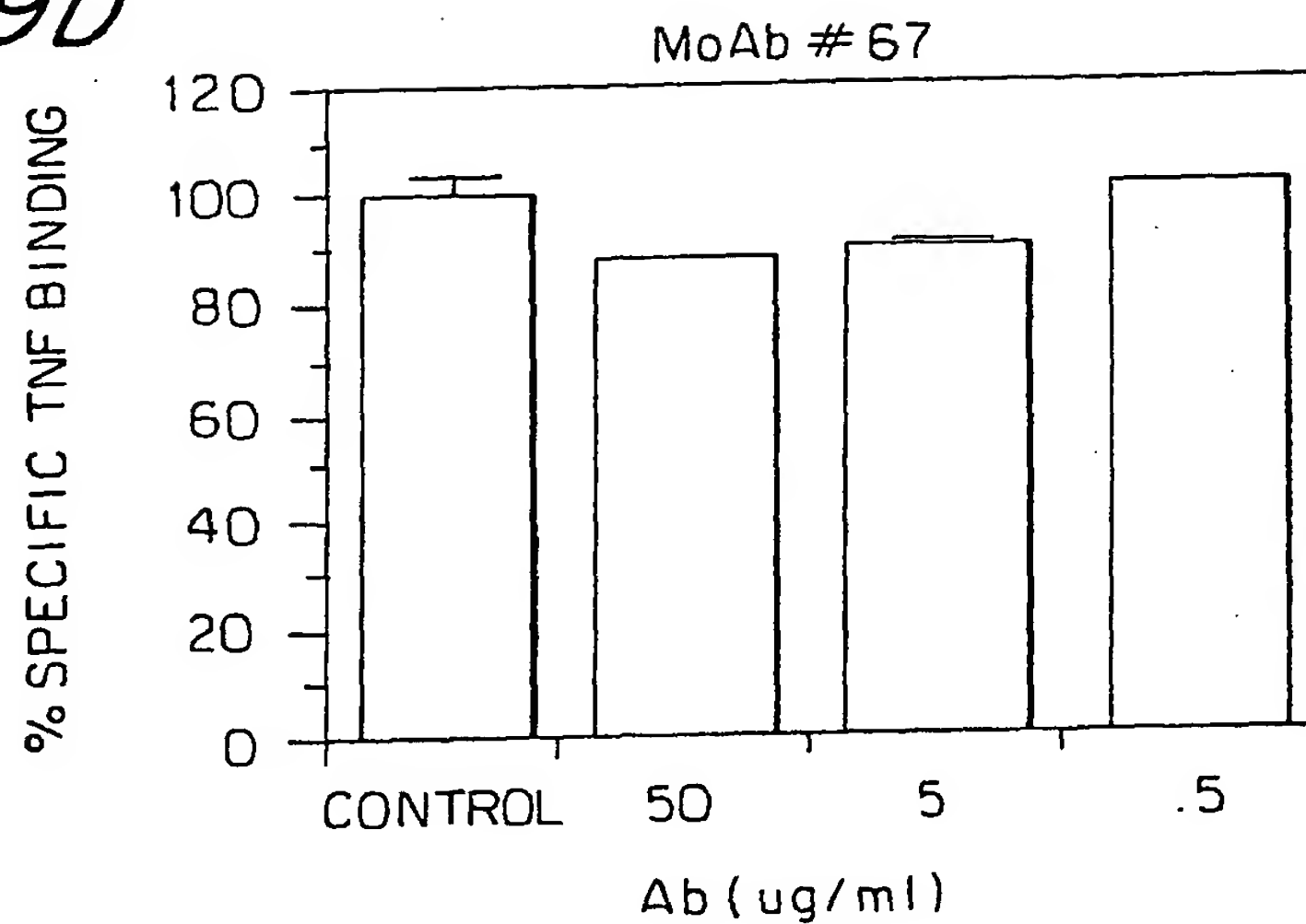


FIG. 9E

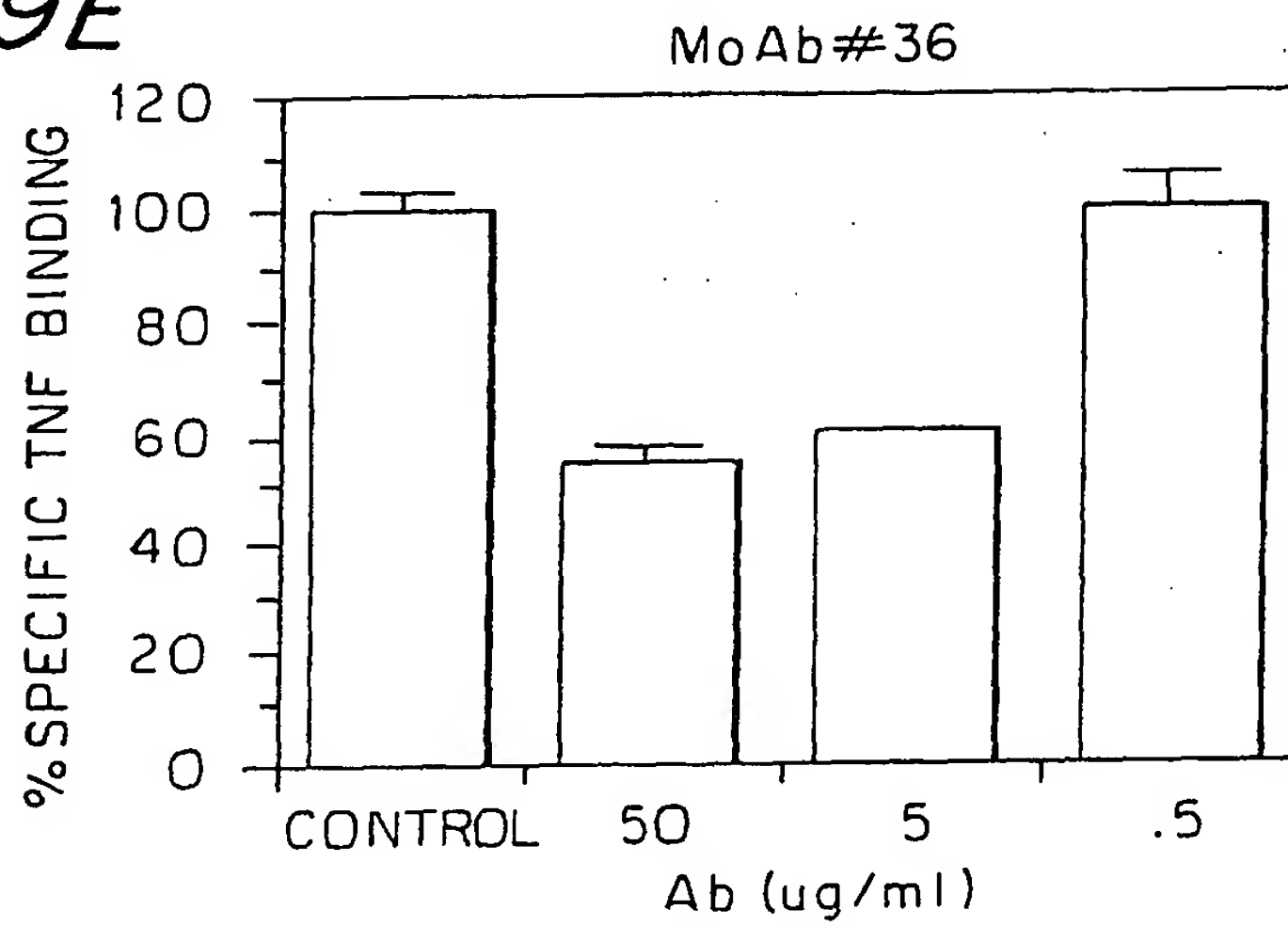


FIG. 9F

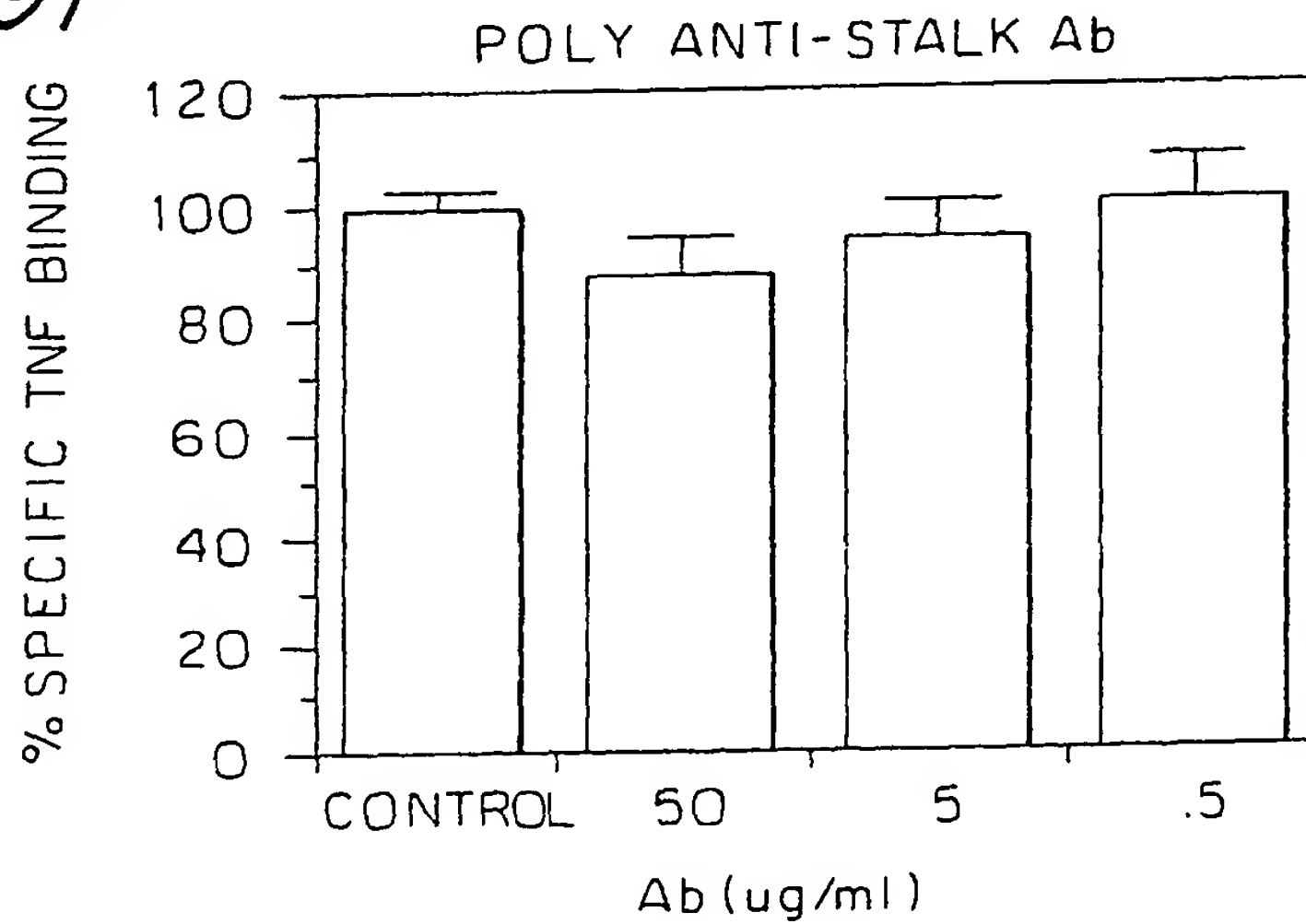
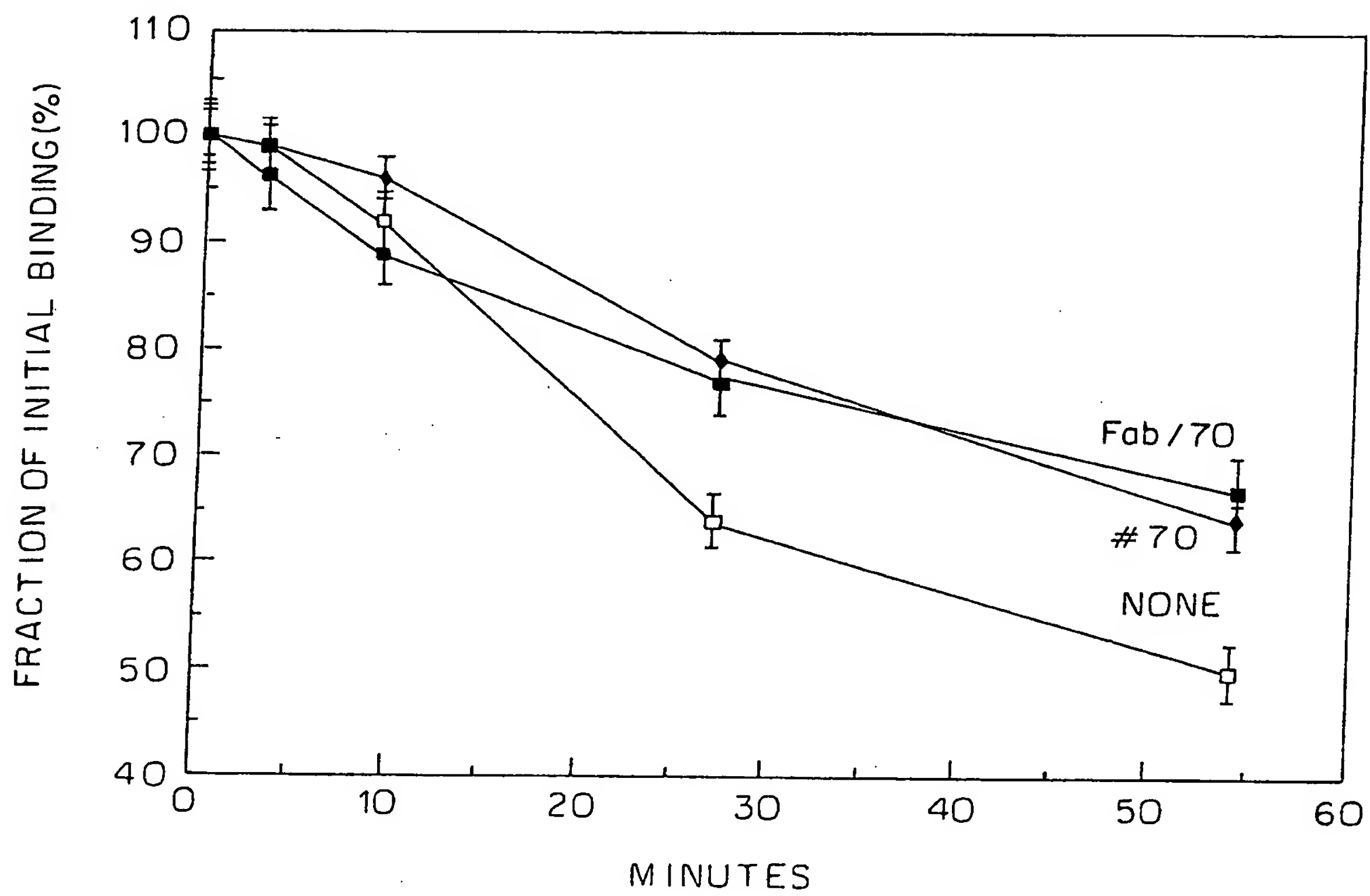


FIG. 10



1/1	#70	GTG AAA	CTG CAG	GAG TCT	GGA CCT	GAG CTG	GTG AAG	CCT GGG	GCC TCA	GTG AAG	ATT TCC
		V K L Q	E S G P	E L G	P E L	V K P	G A S	G A S	V K I	S	
1/1	#32										
1/1	#57	GTG TCC	CTG CAG	GAG TCT	GGG GGA	GGC TTA	GTG CAG	CCT GGA	GGG TCC	CGG AAA	CTC TCC
		V S L Q	E S G G	S S G	G G G	L L G	V Q Q	P G G	S R K	L S	
61/21	#70	TGC AAA	ACT TCT	GGC TTC	GCA TTC	AGT AGT	TCT TGG	ATG AAC	TGG GTG	AGG CAG	AGG CCT
		C K T S	G C F A	F F A	S S H	S S H	S W M	N N	W V R	Q Q R	P
61/21	#32	TGC AAA	GCT TCT	GGC TAC	GCA TTC	AGT AGT	CAC TCT	TGG ATG	TGG GTG	AAG CAG	AGG CCT
		C K A S	G C Y A	F F A	S S H	S S H	S W M	N N	W V K	Q Q R	P
61/21	#57	TGT GCA	GCT TCT	GGA TTC	ACT TTC	AGT AGT	TTT GGA	ATG CAC	TGG GTT	CGT CAG	GCT CCA
		C A A S	G C F T	F T F	S S S	S S S	F G M	H H	W V R	Q Q A	P
121/41	#70	GGA CAG	GGT CTT	GAA TGG	ATT GGA	CGG ATT	TAT CCT	GGA GAT	GGA AAT	ACT GAT	TAC CCT
		G Q G L	E G I W	I I G	R R G	I I G	Y P G	D D G	N T D	Y Y N	
121/41	#32	GGA AAG	GGT CTT	GAG TGG	ATT GGA	CGG ATT	CAT CCT	GGA GAT	GAC ACT	GAC TAC	AAT
		G K G L	E G I W	I I G	R R G	I I G	H P G	D D G	T D T	Y Y N	
121/41	#57	GAG AAG	GGG CTG	GAG TGG	GTC GCA	TAC ATT	AGT AGT	GGC AGT	ACC CTC	CAC TAT	GCA
		E K G L	E G V W	V V A	Y Y A	I I Y	S S S	S S S	T L H	Y Y A	

FIG. 11B

#70	181/61	GGG AAG TTC CAG GGC CAG GCC ACA CTG ACT GCA GAC AAA TCT TCC AGC ACA GCC TAC ATG	211/71
		G K F Q G Q A T L T A D K S S S T A Y M	
	181/61	GGG AAC TTC AGG GGC AAG GCC ACA CTG ACT GCA GAC ACA TCC TCC AGC TCA GCC TAC ATG	211/71
#32		G N F R G K A T L T A D T S S S A Y M	
	181/61	GAC ACA GTG AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT CCC AAG AAC ACG CTG TTC CTG	211/71
		D T V K G R F T I S R D N P K N T L F L	
#70	241/81	CAA CTC TTC AGT CTG ACC TCT GTG GAC TCT GCG GTC TAT TTT TGT GCA CCC GGC CGT TGG	271/91
		Q L F S L T S V D S A V Y F C A P G R W	
	241/81	CAG CTC AGC AGC CTG ACC TCT GTG GAT TCT GCG GTC TAC TTC TGT GCA CCC GGC CGT TGG	271/91
#32		Q L S S L T S V D S A V Y F C A P G R W	
	241/81	CAA ATG AAA CTA CCC TCA CTA TGC TAT GGA CTA CTG GGG CCA AGG GAC CAC GGT CAC CGT	271/91
		Q M K L P S L C Y G L L G P R D H G H R	
#70	301/101	TAC CTC GAA GTC TGG GGC CAA GGG ACC ACC GTC ACC GTC TCC TCA	331/111
		Y L E V W G Q G T T V T V S S	
	301/101	TAC CTC GAG GTC TGG GGC CAA GGG ACC ACC GTC ACC GTC TCC TCA	331/111
#32		Y L E V W G Q G T T V T V S S	
	301/101	CTC CTC A	
		L L	

FIG. 12

61/21	ATG AGC	TGC AAG	TCC AGT	CAG AGC	AGC CTT	TTA ACT	AGT AGC	ACT CAA	AAG AAC	TCT TTG	GCC
M S	C K	C K	S S	Q S	L L	T S	S S	T Q	K N	S L	A
121/41	TGG TAC	CAG CAG	ACA CCA	GGA CAG	TCT CCT	AAA CTT	CTG ATA	TAC TTT	GCA TCC	ACT AGG	
W Y	Q Q	Q T	P P	G Q	S S	P K	L L	I Y	F A	S T	R
181/61	CTA TCT	GGG GTC	CCT GAT	CGC TTC	ATA GGC	AGT GGA	TCT GGG	ACA GAT	TTC ACT	CTT ACC	
L S	G G	V V	P D	R F	I I	S G	S G	T D	F T	L T	
241/81	ATC AGC	AGT GTG	CAG GCT	GAA GAC	CTG GCA	GAT TAC	TTC TGT	CAG CAA	CAT TAT	AGC ACT	
I S	S S	V V	Q A	E D	L A	D Y	F C	Q Q	H Y	S T	
301/101	CCA TTT	ACG TTC	GGC TCG	GGG ACA	AAG TTG	GAA ATA	GAG CGG	GCT GAT	GCT GCA	CCA ACT	
P F	T T	F F	G S	G T	K L	E I	E R	A D	A A	P T	
361/121	GTA TCC	ATC TTC	CCA CCA	TCC A							
V S	I I	F F	P P	S S							

FIG. 13

hu p55 TNF-R (3-42)	VCPQGGKYIHPQNN---SICC-TKCHKGTYLYND---CPGPGQDITDCCR
hu p75 TNF-R (39-76)	TCRLREYD-QTA---QMCC-SKCSFGQHAKVF---CTKTS-DITVCCD
hu FAS (31-67)	QNLGLH-HDGGQF---CH-KPCPPGERKARD---CTVNGDEPDCCV
hu NGF-R (3-37)	ACPTGLYTHSGE---CC-KACNLGEGVAQP---CGA--NQTVCE
hu CDw40 (25-60)	ACREKQYLINSQ---CC-SLCCQPGQKLVSD---CTIEF-TETECL
rat Ox40 (25-60)	NCVKDTYPSGHK---CC-RECQPGHGMVSR---CDHT-RDITVCH
hu p55 TNF-R (43-86)	ECESGSEFTASEHHL-RHCLSC-SKCRKENQVEISSCTVD-RDITVCG
hu p75 TNF-R (77-119)	SCEDSTYTQLWNWV-PECLSCGSRCSDD--QVETQACTRE-QNRICT
hu FAS (68-112)	PCQEGKEYTDKAHFSSKCRRC-RLCDEGHGLEVEINCTRT-QNTKCR
hu NGF-R (38-80)	PCLDSTVTSSDVVSATEPCKPC-TECVGLQSHSAP--CVEA-DDAVCCR
hu CDw40 (61-104)	PCGESEFLDWTWRETN-CHQH-KYCDPNLGLRVQKGTSE-TDTICT
rat Ox40 (61-104)	PC-EPGEFYNEAVNY-DTCKQC-TQCNHRSSELKQNTPT-EDITVCCQ
hu p55 TNF-R (87-126)	-CRKNQYRHYWSENLFQCFNC---SLCLHGT-VHLSCQEK-QNTVC-
hu p75 TNF-R (120-162)	-CRPGWYCA--LSKQEGCRLCAPLRKCRPGFVGVARPGTET-SDVVCK
hu FAS (113-149)	-CKPNFFCN--STVCEHCDDPC---TKCEHGI-IKE-CTLT-SNTKC-
hu NGF-R (81-119)	-CAYGYQD---ETGRCEAC---RVCEAGSGLVFSCQDK-QNTVCE
hu CDw40 (105-144)	-CEEGWHC---TSEACESVLHRSCLVHRSGFVGKQIATGV-SDTICE
rat Ox40 (105-123)	-CRFGTQP-----RQDS-----SHKLGV-----CV
hu p55 TNF-R (127-155)	TCHAGFFLR--ENE---CVSC-SNCKKSL-----ECTK-----LC-
hu p75 TNF-R (163-201)	PCAPGTFSTNTSST-DICRPH-QICN---VVA--IPGNASMDAVCT
hu NGF-R (120-161)	ECPDGTYSDAAHHV-DPCLPC-TVCEDTERQLR--ECTRW-ADAECE
hu CDw40 (145-186)	FCPPVGFFSNVSSAF-EKCHP--TSCETKDLVVQ--QAGTNKTDVVC
rat Ox40 (124-164)	PCPPGHHFSPGSHQ--ACKPW-TNCTLSGKQIR--HPASNSLDTVCE